

SEQUENCE LISTING

<110> HIRANO, Seiko  
YASUEDA, Hisashi

<120> Novel lysine decarboxylase gene and method for  
producing L-lysine

<130> US-109

<150> JP 2003-47185  
<151> 2003-02-25

<160> 26

<170> PatentIn Ver. 2.0

<210> 1  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 1  
gcgagctcag cgcgagtgac tggatatcg a

31

<210> 2  
<211> 31  
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<223> Description of Artificial Sequence: primer

<400> 2

gcggtaccac tgtataaata gcaaaggcaa c

31

<210> 3

<211> 2964

<212> DNA

<213> *Methylphilus methylotrophus*

<220>

<221> CDS

<222> (684)..(2930)

<400> 3

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atgattgagc cgtttgagcc caagcttgcata cgtgagacca atggccagaa gattgttct 120  
tatggcacct cttcttacgg ttacgataatc cgttgtgctg acgaattccg cgtatattacc 180  
aatatcaaca gcaccatagt tgaccccaag caatttgacc cgcatcggtt tgtcgaggtc 240  
tccggcaaag gctattgcgt gattccccctt aactcatttg cactggcgcg cacggtagag 300  
tatttccgta ttccctcgctc tgtactgact gtatgcctcg gcaagtcgac ttatgcgcgt 360  
tgccgcatta tcgtcaacgt caccctttaa gaaccagagt gggaggcta tgtcacacta 420  
gagttcagca acaccacacc gctacccgcc aaaatttatg ctggcgaagg ctgtgcgcaa 480  
gtgcgttgttctt ttgagtctga tgaaatctgt gaaacgagct acaaagaccc tggtggtaaa 540  
taccagggtc aaattggcgt gaccctgcca aaaatataac ggcaacattt aacaataacc 600  
tgacattcac caagggcacg gtgcaaagca aatgcatttctt ctgtgccctt gtgtcttgat 660  
tttagcggtta aaggatttat tgc atg aaa ttt aga ttc cct atc gtc att att 713

Met Lys Phe Arg Phe Pro Ile Val Ile Ile

1 5 10

gac gag gac ttc cgc tcc gag aac tct tcc ggc ctg ggc atc cgt gtg 761

Asp Glu Asp Phe Arg Ser Glu Asn Ser Ser Gly Leu Gly Ile Arg Val

15 20 25

ctg gcg aaa gcc atc gaa gat gag ggc ctg gaa gtg ctt ggc gtc acc 809

Leu Ala Lys Ala Ile Glu Asp Glu Gly Leu Glu Val Leu Gly Val Thr

30 35 40

agc tat ggc gac ctg acc tct ttc gcc cag cag caa agc cgt gca tca 857

Ser Tyr Gly Asp Leu Thr Ser Phe Ala Gln Gln Ser Arg Ala Ser

45 50 55

gcc ttt atc ctg tcg att gat gat gag gaa atc gtt gag gag aaa ccg			905
Ala Phe Ile Leu Ser Ile Asp Asp Glu Glu Ile Val Glu Glu Lys Pro			
60	65	70	
gaa gcc att gag caa ctg cgt aac ttt gtg cag gaa atc cgt tac cgc			953
Glu Ala Ile Glu Gln Leu Arg Asn Phe Val Gln Glu Ile Arg Tyr Arg			
75	80	85	90
aac gag gaa atc ccc att ttc ctg cat ggc gaa acc cgt acc agc cgt			1001
Asn Glu Glu Ile Pro Ile Phe Leu His Gly Glu Thr Arg Thr Ser Arg			
95	100	105	
cac atc cct aac gat gtg ttg cgc gag ttg cac ggc ttt atc cat atg			1049
His Ile Pro Asn Asp Val Leu Arg Glu Leu His Gly Phe Ile His Met			
110	115	120	
aat gaa gac acg cct gag ttt gtg gcg cgc ctg att atc cgc gaa gcc			1097
Asn Glu Asp Thr Pro Glu Phe Val Ala Arg Leu Ile Ile Arg Glu Ala			
125	130	135	
aaa gcc tac ctg gac agc ttg cca ccg ccc ttc aag gca ctc act			1145
Lys Ala Tyr Leu Asp Ser Leu Pro Pro Pro Phe Phe Lys Ala Leu Thr			
140	145	150	
cat tac gcg gct gat ggc tct tat tca tgg cac tgt cct ggt cac tcg			1193
His Tyr Ala Ala Asp Gly Ser Tyr Ser Trp His Cys Pro Gly His Ser			
155	160	165	170
ggt ggc gta gcc ttt ctg aaa tcc cca gtc ggg cag atg ttc cac cag			1241
Gly Gly Val Ala Phe Leu Lys Ser Pro Val Gly Gln Met Phe His Gln			
175	180	185	
ttt ttt ggc gag aac atg ctg cgt gca gac gtg tgt aat gcg gta gat			1289
Phe Phe Gly Glu Asn Met Leu Arg Ala Asp Val Cys Asn Ala Val Asp			
190	195	200	
gaa tta ggc caa tta ctg gat cac acc ggc ccg gtg gcc gct tct gag			1337
Glu Leu Gly Gln Leu Leu Asp His Thr Gly Pro Val Ala Ala Ser Glu			
205	210	215	
cgc aac gct gcg cgc atc tac aac tgc gac cat ttg tac ttt gtc act			1385
Arg Asn Ala Ala Arg Ile Tyr Asn Cys Asp His Leu Tyr Phe Val Thr			
220	225	230	
aac ggc acc tca aca tcg aac aag att gtc tgg aac tca acc gtg gcg			1433
Asn Gly Thr Ser Thr Ser Asn Lys Ile Val Trp Asn Ser Thr Val Ala			
235	240	245	250

ccg ggt gat att gta gtg gtt gat cgt aac tgc cat aaa tcc gta ttg			1481
Pro Gly Asp Ile Val Val Val Asp Arg Asn Cys His Lys Ser Val Leu			
255	260	265	
cac tcc atc att atg acg ggt gcc gtg ccc gtg ttc ctg atg cca acg			1529
His Ser Ile Ile Met Thr Gly Ala Val Pro Val Phe Leu Met Pro Thr			
270	275	280	
cgc aac cat ttc ggc att atc ggg cct atc cca aaa agt gaa ttc gcc			1577
Arg Asn His Phe Gly Ile Ile Gly Pro Ile Pro Lys Ser Glu Phe Ala			
285	290	295	
tgg gaa aac atc cag aaa aag atc gca cgc aac ccg ttt gcc acc gac			1625
Trp Glu Asn Ile Gln Lys Lys Ile Ala Arg Asn Pro Phe Ala Thr Asp			
300	305	310	
aaa aat gcc aag cca cgc gtg ctg acc att aca cag tcc acc tat gat			1673
Lys Asn Ala Lys Pro Arg Val Leu Thr Ile Thr Gln Ser Thr Tyr Asp			
315	320	325	330
ggc gtg ttg tat aac gtg gaa gaa atc aag gaa atg ctg gat ggc aaa			1721
Gly Val Leu Tyr Asn Val Glu Glu Ile Lys Glu Met Leu Asp Gly Lys			
335	340	345	
att gac acc ctg cac ttt gac gaa gcc tgg ttg cca cat gcg acc ttc			1769
Ile Asp Thr Leu His Phe Asp Glu Ala Trp Leu Pro His Ala Thr Phe			
350	355	360	
cat gac ttt tat ggt gac tac cat gcg att ggc gct gac cgc cca cgc			1817
His Asp Phe Tyr Gly Asp Tyr His Ala Ile Gly Ala Asp Arg Pro Arg			
365	370	375	
tgt aaa gaa tcc atg gtg ttc tcc acc cag tcc acg cac aaa cta ttg			1865
Cys Lys Glu Ser Met Val Phe Ser Thr Gln Ser Thr His Lys Leu Leu			
380	385	390	
gca ggc cta agc cag gcc tcg cag att ctg gta cag gat gcc gac cag			1913
Ala Gly Leu Ser Gln Ala Ser Gln Ile Leu Val Gln Asp Ala Asp Gln			
395	400	405	410
aac cgc ctg gac cgt gac gtg ttc aac gaa gcc tat ttg atg cac acc			1961
Asn Arg Leu Asp Arg Asp Val Phe Asn Glu Ala Tyr Leu Met His Thr			
415	420	425	
tcc acc agc ccg caa tat tca att att gcc agc tgc gac gtc gct gct			2009
Ser Thr Ser Pro Gln Tyr Ser Ile Ile Ala Ser Cys Asp Val Ala Ala			
430	435	440	

gcc atg atg gaa gcc cct ggt ggc acc gcc ctg gta gaa gaa tcc ctc		2057
Ala Met Met Glu Ala Pro Gly Gly Thr Ala Leu Val Glu Glu Ser Leu		
445	450	455
aaa gaa gcg ttg gac ttc cgc cgc gcc atg cgc aag gtc gac gaa gaa		2105
Lys Glu Ala Leu Asp Phe Arg Arg Ala Met Arg Lys Val Asp Glu Glu		
460	465	470
tgg ggc aca gac tgg tgg ttt aaa gtc tgg ggt cca act gac ctg tcc		2153
Trp Gly Thr Asp Trp Trp Phe Lys Val Trp Gly Pro Thr Asp Leu Ser		
475	480	485
gaa gac ggc ctg gaa gaa cgt gac gcg tgg atg ctc aaa gcc aat gaa		2201
Glu Asp Gly Leu Glu Glu Arg Asp Ala Trp Met Leu Lys Ala Asn Glu		
495	500	505
cgc tgg cat ggc ttc ggc aac ctg gcc gaa ggc ttt aac atg ctg gat		2249
Arg Trp His Gly Phe Gly Asn Leu Ala Glu Gly Phe Asn Met Leu Asp		
510	515	520
ccg atc aaa gcc acc atc atc acc cca gga cta gac gta gaa ggc gac		2297
Pro Ile Lys Ala Thr Ile Ile Thr Pro Gly Leu Asp Val Glu Gly Asp		
525	530	535
ttt tcc gat gaa ttc ggc atc ccc gct gcc att gtc acc aag tac ctg		2345
Phe Ser Asp Glu Phe Gly Ile Pro Ala Ala Ile Val Thr Lys Tyr Leu		
540	545	550
gct gaa cac ggt gtg atc gtt gaa aaa acc ggt tta tac tca ttc ttt		2393
Ala Glu His Gly Val Ile Val Glu Lys Thr Gly Leu Tyr Ser Phe Phe		
555	560	565
atc atg ttc acc atc ggc att acc aaa ggc cgc tgg aac acg atg gtg		2441
Ile Met Phe Thr Ile Gly Ile Thr Lys Gly Arg Trp Asn Thr Met Val		
575	580	585
gcc gcg tta caa caa ttt aaa gac gac tac gac aag aat cag ccg ctg		2489
Ala Ala Leu Gln Gln Phe Lys Asp Asp Tyr Asp Lys Asn Gln Pro Leu		
590	595	600
tgg aaa gtg ctg cct gag ttt gta cag aaa cat cca cgc tat gaa cgc		2537
Trp Lys Val Leu Pro Glu Phe Val Gln Lys His Pro Arg Tyr Glu Arg		
605	610	615
gta ggc ctg aaa gat cta tgc acg cag att cat gaa gtt tac aaa gct		2585
Val Gly Leu Lys Asp Leu Cys Thr Gln Ile His Glu Val Tyr Lys Ala		
620	625	630

aac gac gta gca cgc ctg acc aca gaa atg tac ctg tct gac atg gtg	2633		
Asn Asp Val Ala Arg Leu Thr Thr Glu Met Tyr Leu Ser Asp Met Val			
635	640	645	650
cca gcc atg aaa ccg acc gat gct ttc tca aaa atg gcg cat cgc aaa	2681		
Pro Ala Met Lys Pro Thr Asp Ala Phe Ser Lys Met Ala His Arg Lys			
655	660	665	
att gaa cgc gta gcc att gat gac ctc gaa ggc cgc gtc act gca gtg	2729		
Ile Glu Arg Val Ala Ile Asp Asp Leu Glu Gly Arg Val Thr Ala Val			
670	675	680	
ctg tta acg ccc tat ccg cca ggc atc ccg ttg ctg atc cct ggc gaa	2777		
Leu Leu Thr Pro Tyr Pro Pro Gly Ile Pro Leu Leu Ile Pro Gly Glu			
685	690	695	
cgc ttt aac aaa gtc att gtg aac tac ctc aag ttt gcg cgc gag ttt	2825		
Arg Phe Asn Lys Val Ile Val Asn Tyr Leu Lys Phe Ala Arg Glu Phe			
700	705	710	
aat gag aaa ttc cca ggc ttt gag acg gat aac cat gga tta gtg aag	2873		
Asn Glu Lys Phe Pro Gly Phe Glu Thr Asp Asn His Gly Leu Val Lys			
715	720	725	730
caa ata gtc gat ggt aaa gcc gtg tat tat gtg gat tgc gtg aag caa	2921		
Gln Ile Val Asp Gly Lys Ala Val Tyr Tyr Val Asp Cys Val Lys Gln			
735	740	745	
gaa gat taa attttttagtt tcactcagca gtttttctac ttag	2964		
Glu Asp			

<210> 4

<211> 748

<212> PRT

<213> *Methylphilus methylotrophus*

<400> 4

Met Lys Phe Arg Phe Pro Ile Val Ile Ile Asp Glu Asp Phe Arg Ser

1	5	10	15
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Glu Asn Ser Ser Gly Leu Gly Ile Arg Val Leu Ala Lys Ala Ile Glu

20	25	30
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Asp Glu Gly Leu Glu Val Leu Gly Val Thr Ser Tyr Gly Asp Leu Thr

35	40	45
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Ser Phe Ala Gln Gln Gln Ser Arg Ala Ser Ala Phe Ile Leu Ser Ile

50	55	60
Asp Asp Glu Glu Ile Val Glu Glu Lys Pro Glu Ala Ile Glu Gln Leu		
65	70	75
Arg Asn Phe Val Gln Glu Ile Arg Tyr Arg Asn Glu Glu Ile Pro Ile		80
85	90	95
Phe Leu His Gly Glu Thr Arg Thr Ser Arg His Ile Pro Asn Asp Val		
100	105	110
Leu Arg Glu Leu His Gly Phe Ile His Met Asn Glu Asp Thr Pro Glu		
115	120	125
Phe Val Ala Arg Leu Ile Ile Arg Glu Ala Lys Ala Tyr Leu Asp Ser		
130	135	140
Leu Pro Pro Pro Phe Phe Lys Ala Leu Thr His Tyr Ala Ala Asp Gly		
145	150	155
Ser Tyr Ser Trp His Cys Pro Gly His Ser Gly Gly Val Ala Phe Leu		160
165	170	175
Lys Ser Pro Val Gly Gln Met Phe His Gln Phe Phe Gly Glu Asn Met		
180	185	190
Leu Arg Ala Asp Val Cys Asn Ala Val Asp Glu Leu Gly Gln Leu Leu		
195	200	205
Asp His Thr Gly Pro Val Ala Ala Ser Glu Arg Asn Ala Ala Arg Ile		
210	215	220
Tyr Asn Cys Asp His Leu Tyr Phe Val Thr Asn Gly Thr Ser Thr Ser		
225	230	235
Asn Lys Ile Val Trp Asn Ser Thr Val Ala Pro Gly Asp Ile Val Val		240
245	250	255
Val Asp Arg Asn Cys His Lys Ser Val Leu His Ser Ile Ile Met Thr		
260	265	270
Gly Ala Val Pro Val Phe Leu Met Pro Thr Arg Asn His Phe Gly Ile		
275	280	285
Ile Gly Pro Ile Pro Lys Ser Glu Phe Ala Trp Glu Asn Ile Gln Lys		
290	295	300
Lys Ile Ala Arg Asn Pro Phe Ala Thr Asp Lys Asn Ala Lys Pro Arg		
305	310	315
Val Leu Thr Ile Thr Gln Ser Thr Tyr Asp Gly Val Leu Tyr Asn Val		320
325	330	335
Glu Glu Ile Lys Glu Met Leu Asp Gly Lys Ile Asp Thr Leu His Phe		

340	345	350
Asp Glu Ala Trp Leu Pro His Ala Thr Phe His Asp Phe Tyr Gly Asp		
355	360	365
Tyr His Ala Ile Gly Ala Asp Arg Pro Arg Cys Lys Glu Ser Met Val		
370	375	380
Phe Ser Thr Gln Ser Thr His Lys Leu Leu Ala Gly Leu Ser Gln Ala		
385	390	395
Ser Gln Ile Leu Val Gln Asp Ala Asp Gln Asn Arg Leu Asp Arg Asp		
405	410	415
Val Phe Asn Glu Ala Tyr Leu Met His Thr Ser Thr Ser Pro Gln Tyr		
420	425	430
Ser Ile Ile Ala Ser Cys Asp Val Ala Ala Ala Met Met Glu Ala Pro		
435	440	445
Gly Gly Thr Ala Leu Val Glu Glu Ser Leu Lys Glu Ala Leu Asp Phe		
450	455	460
Arg Arg Ala Met Arg Lys Val Asp Glu Glu Trp Gly Thr Asp Trp Trp		
465	470	475
Phe Lys Val Trp Gly Pro Thr Asp Leu Ser Glu Asp Gly Leu Glu Glu		
485	490	495
Arg Asp Ala Trp Met Leu Lys Ala Asn Glu Arg Trp His Gly Phe Gly		
500	505	510
Asn Leu Ala Glu Gly Phe Asn Met Leu Asp Pro Ile Lys Ala Thr Ile		
515	520	525
Ile Thr Pro Gly Leu Asp Val Glu Gly Asp Phe Ser Asp Glu Phe Gly		
530	535	540
Ile Pro Ala Ala Ile Val Thr Lys Tyr Leu Ala Glu His Gly Val Ile		
545	550	555
Val Glu Lys Thr Gly Leu Tyr Ser Phe Phe Ile Met Phe Thr Ile Gly		
565	570	575
Ile Thr Lys Gly Arg Trp Asn Thr Met Val Ala Ala Leu Gln Gln Phe		
580	585	590
Lys Asp Asp Tyr Asp Lys Asn Gln Pro Leu Trp Lys Val Leu Pro Glu		
595	600	605
Phe Val Gln Lys His Pro Arg Tyr Glu Arg Val Gly Leu Lys Asp Leu		
610	615	620
Cys Thr Gln Ile His Glu Val Tyr Lys Ala Asn Asp Val Ala Arg Leu		

625                    630                    635                    640  
Thr Thr Glu Met Tyr Leu Ser Asp Met Val Pro Ala Met Lys Pro Thr  
645                    650                    655  
Asp Ala Phe Ser Lys Met Ala His Arg Lys Ile Glu Arg Val Ala Ile  
660                    665                    670  
Asp Asp Leu Glu Gly Arg Val Thr Ala Val Leu Leu Thr Pro Tyr Pro  
675                    680                    685  
Pro Gly Ile Pro Leu Leu Ile Pro Gly Glu Arg Phe Asn Lys Val Ile  
690                    695                    700  
Val Asn Tyr Leu Lys Phe Ala Arg Glu Phe Asn Glu Lys Phe Pro Gly  
705                    710                    715                    720  
Phe Glu Thr Asp Asn His Gly Leu Val Lys Gln Ile Val Asp Gly Lys  
725                    730                    735  
Ala Val Tyr Tyr Val Asp Cys Val Lys Gln Glu Asp  
740                    745

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 5

aaggctgtgc gcaagtgctg ttctttgagt                    30

<210> 6

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

ccagcctaca caatcgctca agacgtgtaa tgcacgcattt gtagtcacca taaaagtcat 60  
ggaa 64

<210> 7

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 7

ggctaattcc catgtcagcc gttaagtgtt ccatgaacta cctcaagttt gcgcgcgagt 60  
ttaa 64

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 8

ggttgtatc agtgtagaca cggttgcaag 30

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 9

gcattacacg tcttgagcga ttgtgttagc 30

<210> 10  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 10  
ggaacactta acggctgaca tggaaattag cc 32

<210> 11  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 11  
aacctgacat tcaccaaggg cacggtgcaa 30

<210> 12  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 12  
tttgcgcaaa agcatcgatt atccttcccc 30

<210> 13  
<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13

gccctgcagg agcgcgagtg actggatatac gga

33

<210> 14

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 14

gccctgcagg ctgtataaat agcaaaggca ac

32

<210> 15

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 15

gcctgcagta aggaaggatt ttccaggagg aacac

35

<210> 16

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 16

gcctgcagaa gcttgcata ccgcataatc cgtcgcaa 38

<210> 17

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 17

aggaaattcc cggttctgga taatgtttt tgccggac 39

<210> 18

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 18

cggatgcatac tagagttaac ctgcagggtg aaattgttat ccgtcacaa ttccacac 58

<210> 19

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 19

catttcctgc aggcaaagga gatgagcgta atggtgatca tgaaaatctt cattacagg 60  
ctgc 64

<210> 20

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 20

ggcgagacta gaagagctcc aaaacccgcg aaaactaacc catcaacatc 50

<210> 21

<211> 711

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(711)

<400> 21

atg gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt 48

Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser

1 5 10 15

ctt tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga 96

Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly

20 25 30

att aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct 144

Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser

35 40 45

gac gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc 192

Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Ser

50	55	60	
aat gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct			240
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala			
65	70	75	80
tac ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac			288
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn			
85	90	95	
aag gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc			336
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro			
100	105	110	
gat gac acg cct ttg ggc ggt tcg gcg gtg gcc act gac acg cgc aac			384
Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn			
115	120	125	
cgg gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag			432
Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys			
130	135	140	
ccc atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat			480
Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr			
145	150	155	160
ttg gac gcg ttt gtg ttt atc ggc ggc gtc ggc gcg caa tac ggc gac			528
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp			
165	170	175	
acc gga cgg tgg att ttc gcc gct ggc gcg ttc gcg gca agc ctg atc			576
Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile			
180	185	190	
tgg ttc ccg ctg gtg ggt ttc ggc gca gca ttg tca cgc ccg ctg			624
Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu			
195	200	205	
tcc agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg			672
Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val			
210	215	220	
atg acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag			711
Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly			
225	230	235	

<211> 236

<212> PRT

<213> *Brevibacterium lactofermentum*

<400> 22

Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser  
1 5 10 15  
Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly  
20 25 30  
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser  
35 40 45  
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser  
50 55 60  
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala  
65 70 75 80  
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn  
85 90 95  
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro  
100 105 110  
Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn  
115 120 125  
Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys  
130 135 140  
Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr  
145 150 155 160  
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp  
165 170 175  
Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile  
180 185 190  
Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu  
195 200 205  
Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val  
210 215 220  
Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly  
225 230 235

<210> 23  
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<213> *Brevibacterium lactofermentum*

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Leu	Leu	Leu	Ser	Ile	Gly	Pro	Gln	Asn	Val	Leu	Val	Ile	Lys	Gln	Gly	
			20				25					30				
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Ile	Lys	Arg	Glu	Gly	Leu	Ile	Ala	Val	Leu	Leu	Val	Cys	Leu	Ile	Ser	
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Asp	Val	Phe	Leu	Phe	Ile	Ala	Gly	Thr	Leu	Gly	Val	Asp	Leu	Leu	Ser	
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Asn	Ala	Ala	Pro	Ile	Val	Leu	Asp	Ile	Met	Arg	Trp	Gly	Gly	Ile	Ala	
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tac	ctg	tta	tgg	ttt	gcc	gtc	atg	gca	gco	aaa	gac	gcc	atg	aca	aac	288
Tyr	Leu	Leu	Trp	Phe	Ala	Val	Met	Ala	Ala	Lys	Asp	Ala	Met	Thr	Asn	
	85				90				95							
aag	gtg	gaa	gco	cca	cag	atc	att	gaa	gaa	aca	gaa	cca	acc	gtg	ccc	336
Lys	Val	Glu	Ala	Pro	Gln	Ile	Ile	Glu	Glu	Thr	Glu	Pro	Thr	Val	Pro	
	100				105				110							
gat	gac	acg	cct	ttg	ggc	gtg	ttc	ggc	ggt	ggc	cac	tga	cacgcgcaac		385	
Asp	Asp	Thr	Pro	Leu	Gly	Val	Phe	Gly	Gly	Gly	His					
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<213> *Brevibacterium lactofermentum*

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Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser

35 40 45

Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser

50 55 60

Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala

65 70 75 80

Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn

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